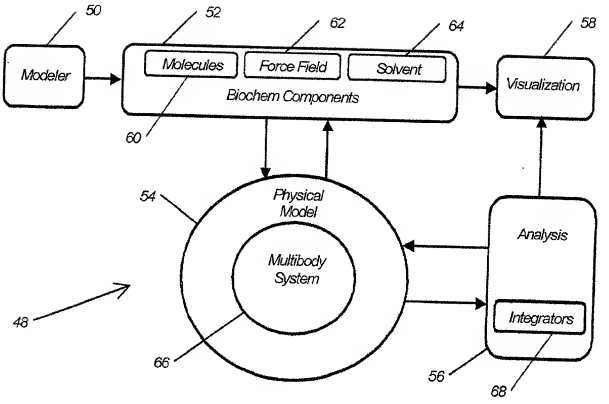

Fig. 1

Residual Form Method to compute ρ_q and ρ_u	Direct Form Method to compute $\dot{q}$ and $\dot{u}$
1. Compute the First Kinematics Calc. and the kinematic residual $\rho_q(k)$ 2. Generate $\hat{T}(k)$, the spatial load balance for each body 3. Compute dynamic residual $\rho_u(k)$	1. Compute $\dot{q}$ using joint specific routines 2. Perform First Kinematics Calc. with $\dot{u}=0$ 3. Generate residuals ρ_u and negate $\rho_u = -\rho_u$ 4. Perform Second Kinematics Calc. 5. Compute $\dot{u}$ using Forward Dynamics

Comparison of Methods

Fig. 5

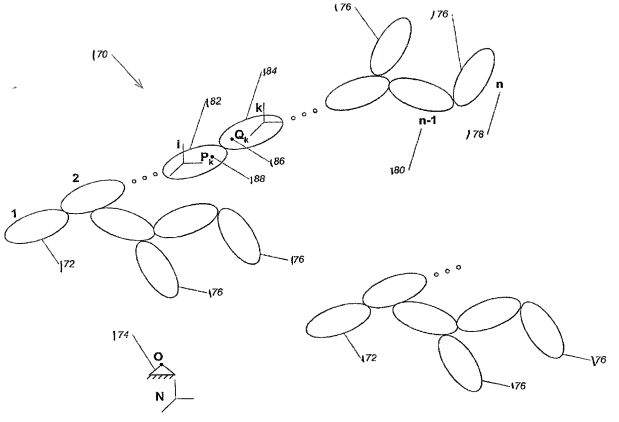
170
176
176
184
182
k
i
Q_k
P_k
186
188
n
n-1
178
180
2
1
172
176
176
174
O
N
172
176
176

Fig. 2

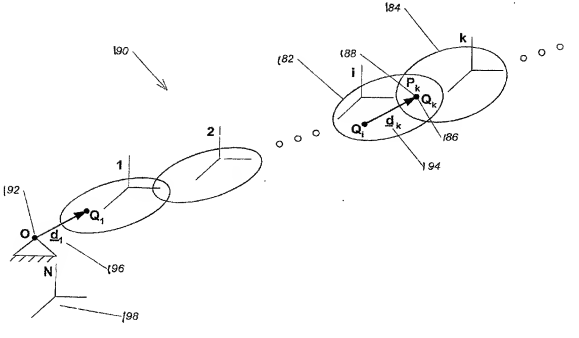
184
k
190
182
188
i
P_k
Q_k
Q_i
g_k
186
194
2
1
192
O
Q_1
g_1
N
196
198

Fig. 3

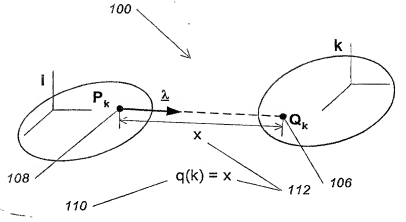

Fig. 4A

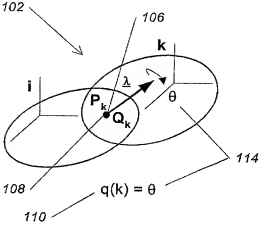

Fig. 4B

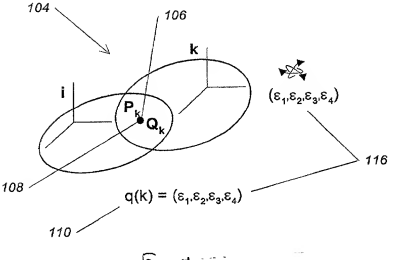

Fig. 4C

Molecule	No. Residues in polypeptide	No. Atoms	Direct Form Approximate Operation Count	Residual Form Approximate Operation Count	Factor of Speed Up
Alanine Dipeptide	2	23	4,991	683	7.31
20-mer Polyalanine	20	257	42,340	5,894	7.24
100-mer Polyalanine	100	1297	207,018	28,973	7.15

Computation Comparison

Fig. 6